AMENDMENTS

Please incorporate the following amendments into the subject application.

In the Claims:

1. (Currently Amended) A method of determining whether a sample includes at least one analyte of interest, said method comprising:

(a) **pre-incubating said sample with a first buffer composition comprising a metal ion chelating polysaccharide;**

(b) contacting said **pre-incubated** sample with a planar array of a plurality of distinct binding agents displayed on a surface of a solid support, wherein ~~**said sample comprises a metal ion chelating polysaccharide and**~~ each of said binding agents at least comprises a specific epitope binding domain of an antibody;

~~**(b)**~~ **(c)** detecting the presence of any resultant binding complexes on said surface to obtain analyte binding data; and

~~**(c)**~~ **(d)** employing said analyte binding data to determine whether said sample includes said at least one analyte of interest.

2. (Canceled)

3. (Previously Presented) The method according to Claim 1, wherein said metal ion chelating polysaccharide comprises polygalactouronate domains.

4. (Original) The method according to Claim 3, wherein said metal ion chelating polysaccharide is a pectin.

5. (Original) The method according to Claim 4, wherein said pectin is apple pectin.

6. (Currently Amended) The method according to Claim 1, wherein said

method further comprises extracting said at least one analyte from a cellular source and labeling said extracted at least one analyte, wherein said extracting and labeling steps employ a **second** buffer composition that is the same.

7. (Currently Amended) The method according to Claim 6, wherein said **second** buffer composition is free of components that include primary amine moieties.

8. (Currently Amended) The method according to Claim 7, wherein said **second** buffer composition has a pH ranging from about 7 to about 12.

9. (Currently Amended) The method according to Claim 8, wherein said **second** buffer composition is capable of extracting at least about 95% of the proteins of an initial cellular source.

10. (Original) The method according to Claim 1, wherein said at least one analyte is a protein.

11. (Original) The method according to Claim 1, wherein said method comprises determining the presence of at least two distinct analytes in said sample.

12. (Original) The method according to Claim 1, wherein said method comprises a plurality of washing steps between said contacting and detecting steps.

13. (Previously Presented) The method according to Claim 1, wherein: (a) said method comprises quantitatively detecting at least two different protein analytes in said sample; (b) said method further comprises extracting said at least one analyte from a cellular source in an extraction buffer and labeling said extracted at least one analyte in a buffer that is the same as said extraction buffer; and (c) wherein said method comprises a plurality of washing steps between said contacting and detecting steps.

14. (Original) The method according to Claim 13, wherein said metal ion chelating polysaccharide comprises polygalactouronate domains.

15. (Original) The method according to Claim 14, wherein said metal ion chelating polysaccharide is a pectin.

16. (Original) The method according to Claim 15, wherein said pectin is apple pectin.

17. (Original) The method according to Claim 13, wherein said method is a method of determining a protein expression profile for said sample.

18. (Original) The method according to Claim 1, wherein said method further comprises a sample fractionating step prior to said contacting step.

19. (Original) The method according to Claim 18, wherein said fractionating step comprises contacting said sample with at least one affinity column.

Claims 20 - 45. (Canceled)